Claims

1. A method for preparing a plurality of different synthetic nucleic acids, comprising the steps:
   (a) provision of a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which are complementary to the nucleic acids to be prepared,
   (b) addition of nucleotide building blocks and of an enzyme which brings about generation of different nucleic acids from the complementary base sequences from (a), and
   (c) detachment of the nucleic acids generated in step (b) and, where appropriate, provision for further operations.

2. A method for preparing a nucleic acid double strand, comprising the steps:
   (a) provision of a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which are complementary to partial sequences of the nucleic acid double strand to be prepared,
   (b) addition of nucleotide building blocks and of an enzyme which brings about generation of partial sequences of the nucleic acid double strand to be prepared from the complementary base sequences from (a), and
   (c) assembly of the partial sequences generated in step b) to give the desired nucleic acid strand.

3. The method as claimed in either of claims 1 or 2, characterized in that
the support is selected from flat supports, porous supports, reaction supports with electrodes,

reaction supports with particles or beads, microfluidic reaction supports which optionally have surface modifications such as gels, linkers, spacers, polymers, amorphous layers or/and 3D matrices, and combinations of the aforementioned supports.

4. The method as claimed in any of claims 1 to 3, characterized in that
a microfluidic support is provided.

5. The method as claimed in any of claims 1 to 4, characterized in that
the nucleic acid fragments from (a) are generated by spatially resolved *in situ* synthesis on the support.

6. The method as claimed in claim 5, characterized in that
the nucleic acid fragments from (a) are synthesized by spatially or/and time-resolved illumination by means of a programmable light source matrix.

7. The method as claimed in claim 6, characterized in that
the spatially or/and time-resolved synthesis takes place in a microfluidic support with one or more fluidic reaction chambers and one or more reaction zones within a fluidic reaction chamber.

8. The method as claimed in any of claims 2 to 7, characterized in that
the assembly of the partial sequences in step (c) takes place at least partly in one or more steps on the support.

9. The method as claimed in any of claims 1 to 8, characterized in that

the nucleic acid fragments from (a) are chosen so that the nucleic acids or partial sequences formed in step (b) can be joined to give nucleic acid double-stranded hybrids.

10. The method as claimed in any of claims 1 to 9, characterized in that a plurality of nucleic acids or partial sequences which form a strand of the nucleic acid double strand are covalently connected together.

11. The method as claimed in claim 10, characterized in that the covalent connection comprises a treatment with ligase or/and a filling-in of gaps in the strands with DNA polymerase.

12. The method as claimed in any of claims 1 to 11, characterized in that step (b) comprises the addition of at least one primer for each position of the support, the primer being complementary to part of the nucleic acid fragment located at this position and step (b) comprising an elongation of the primer.

13. The method as claimed in any of claims 1 to 11, characterized in that double-stranded nucleic acid fragments are provided in step (a), with at least one strand being tethered to the surface of the support.

14. The method as claimed in claim 13, characterized in that step (b) comprises transcription of double-stranded DNA fragments or/and replication of double-stranded RNA fragments.

15. The method as claimed in any of claims 1 to 11, characterized in that

nucleic acid fragments comprising a self-priming 3′ end are provided in step (a), and step (b) comprises elongation of the 3′ end.

16. The method as claimed in claim 15, which comprises elimination of the elongation product.

17. The method as claimed in any of claims 1 to 16, characterized in that
double-stranded, circular nucleic acid fragments are provided in step (a), one strand being tethered to the surface of the support, and the other strand comprising a self-priming 3′ end, and step (b) comprising elongation of the 3′ end.

18. The method as claimed in claim 17, which comprises elimination of the elongation product.

19. The method as claimed in any of claims 1 to 18, characterized in that
the nucleic acid fragments from (a) are generated by:
- provision of capture probes at the positions and
- binding of nucleic acid fragments from a fluid passed over the support to the capture probes,

where the capture probes are complementary to partial regions of the nucleic acid fragments.

20. The method as claimed in any of claims 1 to 19, characterized in that
recognition sequences for specific interaction with molecules such as proteins, nucleic acids, peptides, drugs, saccharides, lipids, hormones or/and organic compounds are present at one or more positions in the sequence of the nucleic acid or of the nucleic acid double strand.

21. The method as claimed in any of claims 1 to 20,

characterized in that
the sequence of the nucleic acid or of the nucleic acid double strands is a naturally occurring sequence, a non-naturally occuring sequence or a combination of these two.

22. The method as claimed in any of claims 1 to 21, characterized in that
the sequence is taken from a database, from a sequencing experiment or from an apparatus for integrated synthesis and analysis of polymers.

23. The method as claimed in any of claims 1 to 22, characterized in that
the nucleotide building blocks may comprise naturally occurring nucleotides, modified nucleotides or mixtures thereof.

24. The method as claimed in any of claims 1 to 23, characterized in that
modified nucleotide building blocks are used for labeling and subsequent detection of the nucleic acids or of the joined nucleic acid double strands.

25. The method as claimed in claim 24, characterized in that
molecules to be detected in a light-dependent or/and electrochemical manner are used as labeling groups.

26. The use of nucleic acids or nucleic acid double strands prepared by the method as claimed in any of claims 1 to 25 for therapeutic or pharmacological purposes.

27. The use of nucleic acids or nucleic acid double strands prepared by the method as claimed in any of claims 1 to 25 for diagnostic purposes.

28. The use as claimed in either of claims 26 to 27, comprising a transfer into effector cells.

29. The use of nucleic acids or nucleic acid double strands prepared by the process as claimed in any of claims 1 to 25, where they are stabilized, condensed or/and topologically manipulated during a stepwise combination and joining or subsequent thereto.

30. The use as claimed in claim 29 where the stabilization, condensation or/and topological manipulation is effected by functional molecules such as histones or topoisomerases.

31. The use of nucleic acids or nucleic acid double strands prepared by the method as claimed in any of claims 1 to 25 as propagatable cloning vector where the propagatable cloning vector can serve in suitable target cells for transcription, for expression of the transcribed sequence, and where appropriate for the isolation of expressed gene products.